PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/089,678

DATE: 07/29/2002
TIME: 08:47:14

Input Set : **A:\PTO.VSK.txt**
Output Set: **N:\CRF3\07292002\J089678.raw**

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   3 <110> APPLICANT: ASANO, Shinichiro
   5 <120> TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE
PROTEIN, AND
   6       NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
   8 <130> FILE REFERENCE: Q68821
  10 <140> CURRENT APPLICATION NUMBER: 10/089,678
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.C--> 11 **<141> CURRENT FILING DATE: 2002-05-02**

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  13 <150> PRIOR APPLICATION NUMBER: JP 2000-236140
  14 <151> PRIOR FILING DATE: 2000-08-03
  16 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06660
  17 <151> PRIOR FILING DATE: 2001-08-02
  19 <160> NUMBER OF SEQ ID NOS: 3
  21 <170> SOFTWARE: PatentIn version 3.1
  23 <210> SEQ ID NO: 1
  24 <211> LENGTH: 1167
  25 <212> TYPE: PRT
  26 <213> ORGANISM: Bacillus thuringiensis
  28 <400> SEQUENCE: 1
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  35              20                  25                  30
  38 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
  39          35                  40                  45
  42 Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
  43      50                  55                  60
  46 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
  47 65                  70                  75                  80
  50 Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser
  51                  85                  90                  95
  54 Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
  55                  100                 105                 110
  58 Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
  59              115                 120                 125
  62 Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
  63      130                 135                 140
  66 Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
  67 145                 150                 155                 160
  70 Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
  71              165                 170                 175
  74 Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
  75              180                 185                 190
  78 Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
  79          195                 200                 205
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82 Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
83     210               215               220
86 Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
87 225               230               235               240
90 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
91               245               250               255
94 Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
95               260               265               270
98 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
99         275               280               285
102 Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu
103     290               295               300
106 Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe
107 305               310               315               320
110 Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu
111               325               330               335
114 Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile
115               340               345               350
118 Glu Phe Tyr Thr Thr Arg Ala Gly Leu Pro Leu Asn Asn Thr Glu Tyr
119         355               360               365
122 Leu Glu Tyr Trp Val Gly His Ser Ile Lys Tyr Lys Asn Thr Asn Ala
123     370               375               380
126 Ser Ser Ala Leu Glu Arg Asn Tyr Gly Thr Ile Thr Ser Asn Lys Ile
127 385               390               395               400
130 Lys Tyr Tyr Asp Leu Ala Asn Lys Asp Ile Phe Gln Val Arg Ser Leu
131               405               410               415
134 Gly Ala Asp Leu Ala Asn Tyr Tyr Ala Gln Val Tyr Gly Val Pro Tyr
135         420               425               430
138 Ala Ser Phe Thr Leu Leu Asp Lys Asn Thr Gly Ser Gly Ser Val Gly
139     435               440               445
142 Gly Phe Thr Tyr Ser Lys Pro His Thr Thr Met Gln Val Cys Thr Gln
143     450               455               460
146 Asn Tyr Asn Thr Ile Asp Glu Ile Pro Pro Glu Asn Glu Pro Leu Ser
147 465               470               475               480
150 Arg Gly Tyr Ser His Arg Leu Ser His Ile Thr Ser Tyr Ser Phe Ser
151               485               490               495
154 Lys Asn Ala Ser Ser Pro Ala Arg Tyr Gly Asn Leu Pro Val Phe Ala
155         500               505               510
158 Trp Thr His Arg Ser Ala Asp Val Thr Asn Thr Val Tyr Ser Asp Lys
159     515               520               525
162 Ile Thr Gln Ile Pro Val Val Lys Ala His Thr Leu Val Ser Gly Thr
163     530               535               540
166 Thr Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asn Ile Leu Lys Arg
167 545               550               555               560
170 Thr Ser Ser Gly Pro Leu Ala Tyr Thr Ser Val Ser Val Lys Ser Pro
171               565               570               575
174 Leu Ser Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn
175         580               585               590
178 Leu Arg Leu Phe Val Thr Ile Ser Gly Thr Arg Ile Tyr Ser Ile Asn
```

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179         595                  600                  605
182 Val Asn Lys Thr Met Asn Lys Gly Asp Asp Leu Thr Phe Asn Thr Phe
183     610                  615                  620
186 Asp Leu Ala Thr Ile Gly Thr Ala Phe Thr Phe Ser Asn Tyr Ser Asp
187 625                  630                  635                  640
190 Ser Leu Thr Val Gly Ala Asp Ser Phe Ala Ser Gly Gly Glu Val Tyr
191                  645                  650                  655
194 Val Asp Lys Phe Glu Leu Ile Pro Val Asn Ala Thr Phe Glu Ala Glu
195                  660                  665                  670
198 Glu Asp Leu Asp Val Ala Lys Lys Ala Val Asn Gly Leu Phe Thr Ser
199         675                  680                  685
202 Lys Lys Asp Ala Leu Gln Thr Ser Val Thr Asp Tyr Gln Val Asn Gln
203     690                  695                  700
206 Ala Ala Asn Leu Val Glu Cys Leu Ser Asp Glu Leu Tyr Pro Asn Glu
207 705                  710                  715                  720
210 Lys Arg Met Leu Trp Asp Ala Val Lys Glu Ala Lys Arg Leu Val Gln
211                  725                  730                  735
214 Ala Arg Asn Leu Leu Gln Asp Thr Gly Phe Asn Arg Ile Asn Gly Glu
215                  740                  745                  750
218 Asn Gly Trp Thr Gly Ser Thr Gly Ile Glu Val Ala Glu Gly Asp Val
219         755                  760                  765
222 Leu Phe Lys Asp Arg Ser Leu Arg Leu Thr Ser Ala Arg Glu Ile Asp
223     770                  775                  780
226 Thr Glu Thr Tyr Pro Thr Tyr Leu Tyr Gln Gln Ile Asp Glu Ser Leu
227 785                  790                  795                  800
230 Leu Lys Pro Tyr Thr Arg Tyr Lys Leu Lys Gly Phe Ile Gly Ser Ser
231                  805                  810                  815
234 Gln Asp Leu Glu Ile Lys Leu Ile Arg His Arg Ala Asn Gln Ile Val
235         820                  825                  830
238 Lys Asn Val Pro Asp Asn Leu Leu Pro Asp Val Leu Pro Val Asn Ser
239         835                  840                  845
242 Cys Gly Gly Ile Asp Arg Cys Ser Glu Gln Gln Tyr Val Asp Ala Asn
243     850                  855                  860
246 Leu Ala Leu Glu Asn Asn Gly Glu Asn Gly Asn Met Ser Ser Asp Ser
247 865                  870                  875                  880
250 His Ala Phe Ser Phe His Ile Asp Thr Gly Glu Ile Asp Leu Asn Glu
251                  885                  890                  895
254 Asn Thr Gly Ile Trp Val Val Phe Lys Ile Pro Thr Thr Asn Gly Tyr
255                  900                  905                  910
258 Ala Thr Leu Gly Asn Leu Glu Leu Val Glu Glu Gly Pro Leu Ser Gly
259         915                  920                  925
262 Glu Thr Leu Glu Arg Ala Gln Gln Gln Glu Gln Gln Trp Gln Asp Lys
263     930                  935                  940
266 Met Ala Arg Lys Arg Gly Ala Ser Glu Lys Ala Tyr Tyr Ala Ala Lys
267 945                  950                  955                  960
270 Gln Ala Ile Asp Arg Leu Phe Ala Asp Tyr Gln Asp Gln Lys Leu Asn
271                  965                  970                  975
274 Ser Gly Val Glu Met Ser Asp Met Leu Ala Ala Gln Asn Leu Val Gln
275                  980                  985                  990
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278 Ser Ile Pro Tyr Val Tyr Asn Asp  Ala Leu Pro Glu Ile  Pro Gly Met
279         995                 1000                 1005
282 Asn Tyr  Thr Ser Phe Thr Glu  Leu Thr Asn Arg Leu  Gln Gln Ala
283     1010                 1015                 1020
286 Trp Asn  Leu Tyr Asp Leu Arg  Asn Ala Ile Pro Asn  Gly Asp Phe
287     1025                 1030                 1035
290 Arg Asn  Gly Leu Ser Asp Trp  Asn Ala Thr Ser Asp  Val Asn Val
291     1040                 1045                 1050
294 Gln Gln  Leu Ser Asp Thr Ser  Val Leu Val Ile Pro  Asn Trp Asn
295     1055                 1060                 1065
298 Ser Gln  Val Ser Gln Gln Phe  Thr Val Gln Pro Asn  Tyr Arg Tyr
299     1070                 1075                 1080
302 Val Leu  Arg Val Thr Ala Arg  Lys Glu Gly Val Gly  Asp Gly Tyr
303     1085                 1090                 1095
306 Val Ile  Ile Arg Asp Gly Ala  Asn Gln Thr Glu Thr  Leu Thr Phe
307     1100                 1105                 1110
310 Asn Ile  Cys Asp Asp Asp Thr  Gly Val Leu Ser Ala  Asp Gln Thr
311     1115                 1120                 1125
314 Ser Tyr  Ile Thr Lys Thr Val  Glu Phe Thr Pro Ser  Thr Glu Gln
315     1130                 1135                 1140
318 Val Trp  Ile Asp Met Ser Glu  Thr Glu Gly Val Phe  Asn Ile Glu
319     1145                 1150                 1155
322 Ser Val  Glu Leu Val Leu Glu  Glu Glu
323     1160                 1165
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326 <210> SEQ ID NO: 2
327 <211> LENGTH: 3504
328 <212> TYPE: DNA
329 <213> ORGANISM: Bacillus thuringiensis
331 <220> FEATURE:
332 <221> NAME/KEY: exon
333 <222> LOCATION: (1)..(3501)
334 <223> OTHER INFORMATION:
337 <400> SEQUENCE: 2

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338 atg agt cca aat aat caa aat gaa tat gaa att cta gat gct tca tca        48
339 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Leu Asp Ala Ser Ser
340 1               5                  10                 15
342 tct act tct gta tcc gat aat tct gtt aga tac cct tta gca aac gat        96
343 Ser Thr Ser Val Ser Asp Asn Ser Val Arg Tyr Pro Leu Ala Asn Asp
344             20                 25                 30
346 caa acg acc aca tta caa aac atg aac tat aaa gat tat ctg aga atg       144
347 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
348         35                 40                 45
350 tct gag gga gag aat cct gaa tta ttt gga aat ccg gag acg ttt att       192
351 Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
352     50                 55                 60
354 agt tca tct acg gtt caa act gga att ggc att gtt ggt caa gta ctg       240
355 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
356 65                 70                 75                 80
358 ggg gct tta ggg gtt cca ttt gct gga cag ata gct agt ttt tat agt       288
```

```
359 Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser
360               85                   90                   95
362 ttc att gtc ggt caa tta tgg cca tca agt acc gtg agt gta tgg gaa    336
363 Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
364               100                 105                 110
366 atg att atg aaa caa gtg gaa gat cta att gat caa aaa ata aca gat    384
367 Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
368               115                 120                 125
370 tct gta agg aaa aca gcg ctt gca gga cta caa gga tta gga gat ggc    432
371 Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
372       130                 135                 140
374 tta gac gta tat cag aaa tca ctt aag aat tgg ctg gaa aat cgt aat    480
375 Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
376 145                 150                 155                 160
378 gat aca aga gct aga agt gtt gtg gtg acc caa tat ata gct tta gag    528
379 Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
380               165                 170                 175
382 ctt gat ttt gtt gct aaa atc cca tct ttt gca ata tct gga cag gaa    576
383 Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
384               180                 185                 190
386 gta cca tta tta tca gtg tat gca caa gca gcg aat tta cat ttg cta    624
387 Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
388               195                 200                 205
390 tta tta cga gat gct tcc att ttt gga gca gag tgg gga ttc aca cca    672
391 Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
392       210                 215                 220
394 gga gaa att tcc aca ttt tat gat cgt cag gtg aca cgt acc gcc caa    720
395 Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
396 225                 230                 235                 240
398 tac tcg gat tat tgt gta aag tgg tat aac act ggc tta gat aaa tta    768
399 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
400               245                 250                 255
402 aaa ggt acg aat gct gca agt tgg ctg aag tat cac caa ttc cga aga    816
403 Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
404               260                 265                 270
406 gaa atg aca tta ctg gta tta gat tta gta gcg tta ttt cca aac tat    864
407 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
408       275                 280                 285
410 gac aca cgt acg tat cca atc gaa aca acg gcc caa ctt aca cgg gaa    912
411 Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu
412       290                 295                 300
414 gtg tat aca gat cca ata gta ttt aac aga gaa aca agt ggt gga ttt    960
415 Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe
416 305                 310                 315                 320
418 tgt agg cgt tgg tca ctt aac agt gat att tct ttt tca gaa gtc gaa    1008
419 Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu
420               325                 330                 335
422 agc gct gta att cgt tca cca cac cta ttt gat ata ctc agt gaa ata    1056
423 Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date